

A

Human	MSAGDAVCTGWLKSPPERKLQRYAWRKRFVLRGRMSGNPDVLEYRKNHSSKPIRVI	60
Murine	MSTGDTVCMGWLKSPPERKLQRYAWRKRFVLRGRMSGNPDVLEYRKNHSHKPIRVI	60
	**:**:* ***:*****.*****.*****	
Human	DLSECAVWKHVGPSFVRKEFQNNFVFIVKTTSRFTYLVAKTEQEMQVWVHSISQVCN	120
Murine	DLSECTVWKHAGPGFIRKEFQKNFVFIVKTTSRFTYLVAKTEEEMQVWVHSISQVCN	120
	*****:**:*:*:**:*****.*****.*****.*****.*****	
Human	LEDGADSMESLSYTPSSLQPSASSLLTAHAASSSLPRDDPNTNAVATEETRSESELLFL	180
Murine	LEDGADSMESLSHMPSSFQPSASSLHTVHVANSALLKDDGNTNSVTEETRRESEFLFL	180
	*****:**:*:**:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*	
Human	PDYLVLSNCETGRLHHTSLPTRCDSWSNSDRSLEQASFDDVFVDCLQPLPSSHLVHPSCH	240
Murine	PDYLILSNCETGRLHHASLPTRCDSWSNSNHSLAQTSFDDVFVDGLQPFISNNLVHPLHH	240
	*****:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:*	
Human	GSGAQEVPSRPPQAALIWSREINGPPRDHLSSSPLLESSLSSTIQVDKNQGSPLCGAKEL	300
Murine	GKVSQDFPSIRPQASLIWNREINGPSRNLSSSPLLESSLNPTVHVEEKQVSLPSGVKEL	300
	*.*:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:*	
Human	DIMSNTPPPRPPKPSHLSERRQEE--WSTHSGSKKPECTLVPRRISLSGLDNMRTWKADV	358
Murine	NIMSNIPPPRPPKPSYLSEQRQDQPLLTGHSSNKKPGYTMVPRRISLSGLDHVGSWKGDV	360
	:**** *****:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:	
Human	EGQSLRHRDKRLSLNLPCRFS	418
Murine	QSQSLRHRDKRLSLNLPCRFS	420
	:*****:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:	
Human	SGSISSPLPELPANLEPPPVNRDLKPQKRSRPPPLDLRNLIIREHASLTRTRTVPCSR	478
Murine	S----SMLPELPADLEPPPVNRNLKPQKRSRPPPLDSRNLSTIQEHTSLTRTYTVPCNRT	476
	* * *****:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:	
Human	SFLSPERNGINARSFFANPVSREDEES	527
Murine	SFLSPQRNGINCARLFSTPSEEEEEEEEEEEEEEEEEKYIQMEEYGTVSSLSRSALSWTK	536
	*****:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:	
Human	KFSLDYLDLDFNSASPAPMQKLLLSEEQRVDYVQVDEQKTQALQSTKQEWTDERQSKV	586
Murine	KFSLDYLDLDFNSTSPAPVQKLLLSEEQRVDYVQVDEQKTQAFRSTKQAWTDERQSKV	595
	*****:**:*:**:*:**:*:**:*:**:*:**:*:**:*:**:	

Figure 1A

**B**

The figure displays three schematic diagrams of protein domain architectures, labeled Gab1, Gab3, and Gab2. Each diagram shows a horizontal bar representing the protein, with various domains and features indicated by symbols and labels.

- Gab1:** The protein is 695 aa long. It starts with a PH domain (black box). Following the PH domain, there are several tyrosine (Y) phosphorylation sites. A proline (P) is located near the first SH2 domain (white box). The protein ends with a tail region containing more tyrosine sites. A scale bar indicates 50 aa.
- Gab3:** The protein is 595 aa long. It starts with a PH domain (black box). It contains two SH2 domains (white boxes). Tyrosine (Y) phosphorylation sites are distributed throughout the protein, including on the SH2 domains. Proline (P) sites are also indicated.
- Gab2:** The protein is 666 aa long. It starts with a PH domain (black box). It contains three SH2 domains (white boxes). Tyrosine (Y) phosphorylation sites are distributed throughout the protein, including on the SH2 domains. Proline (P) sites are also indicated.

C

Gab3	MSTG--D-TVCMGWLKSPPERKLQRYAWRKRWFVLRGR	37
Gab2	MSGGGGDDVVCTGWLKSPPEKKLRRYAWKKRWFILRSGR	40
Gab1	MSGG--E-VVCSGWLKSPPEKKLKRYAWKRWFVLRSGR	37
	** * : . ** *** *****: **: *****: : *****: ** **	
Gab3	MSGNPDVLEYYRNKHSNKPIRVIDLSECTVWKHAGPGFIR	77
Gab2	MSGDPDVLEYYKNEHSKKPLRIINLNLCEQVD-AGLTFNK	79
Gab1	LTGDPDVLEYYKNDHAKKPIRIIDLNLCCQVD-AGLTFNK	76
	: : *: *****: * . *: : *: *: *: * . ** *	
Gab3	KEFQKNFVFIVKTTSRTFYLVAKTEEEMQVWVHSISQVCN	117
Gab2	KELQDSFVFDIKTSERTFYLVAETEAMDNKWVQSICQICG	119
Gab1	KEFENSYIFDINTIDRIFYLVADSEEDMNKWVRCICDICG	116
	** : : : : * : : * . * *****: * : : : ** : : * : : *	

Figure 1B and C